

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101 527,156 A  
Source: IFW16  
Date Processed by STIC: 4/12/07

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/527,156A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11        Use of <220>     ~~Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.~~  
                          Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please **explain source of genetic material** in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 04/12/2007

PATENT APPLICATION: US/10/527,156A

TIME: 11:27:19

Input Set : A:\SAE-0031 Sequence Listing.txt

Output Set: N:\CRF4\04122007\J527156A.raw

3 <110> APPLICANT: Japan Science and Technology Agency (Assignee)  
 4 Masahiko Sisido (Inventor)  
 5 Keiko Ninomiya (Inventor)  
 7 <120> TITLE OF INVENTION: Method of Aminoacylating tRNA  
 9 <130> FILE REFERENCE: SAE-0031  
 11 <140> CURRENT APPLICATION NUMBER: 10/527,156A  
 12 <141> CURRENT FILING DATE: 2005-03-09  
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/011391  
 15 <151> PRIOR FILING DATE: 2003-09-05  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: PatentIn version 3.2  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 77  
 23 <212> TYPE: RNA  
 24 <213> ORGANISM: Yeast  
 26 <220> FEATURE:  
 W--> 27 <221> NAME/KEY:  
 28 <223> OTHER INFORMATION: tRNA (Phe CGGG)  
 30 <400> SEQUENCE: 1  
 31 gcggaauuag cucaguuggg agagcgccag acucccgaaug cuggaggucc uguguucgau 60  
 33 ccacagaauu cgcacca 77  
 36 <210> SEQ ID NO: 2  
 37 <211> LENGTH: 6  
 38 <212> TYPE: DNA  
 C--> 39 <213> ORGANISM: Artificial Sequence  
 41 <220> FEATURE:  
 42 <223> OTHER INFORMATION: Protein Nucleic Acid  
 44 <400> SEQUENCE: 2  
 45 tgggtgc 6  
 48 <210> SEQ ID NO: 3  
 49 <211> LENGTH: 9  
 50 <212> TYPE: DNA  
 51 <213> ORGANISM: Artificial Sequence  
 53 <220> FEATURE:  
 54 <223> OTHER INFORMATION: Protein Nucleic Acid  
 56 <400> SEQUENCE: 3  
 57 ttttgcatt 9  
 60 <210> SEQ ID NO: 4  
 61 <211> LENGTH: 18  
 62 <212> TYPE: DNA  
 63 <213> ORGANISM: Artificial Sequence  
 65 <220> FEATURE:  
 66 <223> OTHER INFORMATION: DNA Template

Do Not Copy  
 Out of Context Needed  
 (Pg. 1-2) @

Artificial

PLS explain source  
 of genetic material

What is the source of  
 genetic material?

PLS see item # 11 on error  
 summary sheet.

Same error

## RAW SEQUENCE LISTING

DATE: 04/12/2007

PATENT APPLICATION: US/10/527,156A

TIME: 11:27:19

Input Set : A:\SAE-0031 Sequence Listing.txt

Output Set: N:\CRF4\04122007\J527156A.raw

68 &lt;220&gt; FEATURE:

69 &lt;221&gt; NAME/KEY: MISC\_FEATURE

70 &lt;222&gt; LOCATION: (10)..(10)

71 &lt;223&gt; OTHER INFORMATION: Spacer

73 &lt;400&gt; SEQUENCE: 4

W--&gt; 74 aatgcaaaan tgggtgcga

18

Same  
error

↗ pls see item #11 on  
error summary sheet

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 04/12/2007  
PATENT APPLICATION: US/10/527,156A      TIME: 11:27:20

Input Set : A:\SAE-0031 Sequence Listing.txt  
Output Set: N:\CRF4\04122007\J527156A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 10

## VERIFICATION SUMMARY

DATE: 04/12/2007

PATENT APPLICATION: US/10/527,156A

TIME: 11:27:20

Input Set : A:\SAE-0031 Sequence Listing.txt

Output Set: N:\CRF4\04122007\J527156A.raw

L:27 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:39 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0